CLAIMS

1. A method for determining an original animal species in a sample liable to contain an ingredient obtained from at least said species, characterized in that:

a) a nucleic acid fraction obtained from said sample is provided,

b) at least one reagent specific for the animal species is provided, chosen from the group consisting of

- the reference sequences SEQ ID Nos 1 to 232, and Nos 242 to 261,
- the sequences complementary to each of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261, respectively, the complementarity meaning any sequence capable of hybridizing, at a temperature of between 20 and 70°C, in saline solution at a concentration of approximately 0.5 to 1 M, with any one of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261,
- the sequences homologous to each of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261 and of the sequences complementary to each of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261, respectively, the homology meaning any sequence, for example fragment, comprising a series of at least 5 contiguous nucleotides included in any one of said sequences, and exhibiting at least 70% identity with said any sequence,

c) the nucleic acid fraction and said reagent are brought into contact, and

d) any signal or item of information resulting from the specific reaction between said reagent and the nucleic acid fraction, characterizing the presence in said sample of said original animal species, is determined by means of detection.

2. The method as claimed in claim 1, characterized in that a set comprising a multiplicity of said reagents specific for the same original species and/or for respectively different original animal species is provided; and a multiplicity of signals or items of information characterizing the presence in said sample of the same original animal species and/or of several respectively different original animal species is determined.

3. A nucleotide sequence characterized in that it is chosen from the group consisting of:

a) the reference sequences SEQ ID Nos 1 to 232, and Nos 242 to 261,

b) the sequences complementary to each of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261, respectively, the complementarity meaning any sequence capable of hybridizing, at a temperature of between 20 and 70°C, in saline solution at a concentration of approximately 0.5 to 1 M, with any one of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261,

c) the sequences homologous to each of the sequences SEQ ID Nos 1 to 232, and Nos 242 to 261, and of the sequences according to b), respectively, the homology meaning any sequence, for example fragment, comprising a series of at least 5 contiguous nucleotides included in any one of said sequences, and exhibiting at least 70% identity with said any sequence.

4. The use of a sequence as claimed in claim 3, for determining at least one original animal species in a sample liable to contain an ingredient obtained from at least said animal species.

5. A probe for determining at least one original animal species, comprising at least one identifying nucleotide sequence as claimed in claim 3.

6. A primer for the specific amplification of a nucleic acid from an original animal species, comprising at least one identifying nucleotide sequence as claimed in claim 3.

7. A reagent for determining at least one original animal species, comprising a solid support, which may or may not be divided up, to which a nucleotide sequence as claimed in claim 3 is attached.

8. A biochip comprising a solid support comprising a developed surface, on which a multiplicity of nucleotide sequences as claimed in claim 3 is arranged and attached, according to a predetermined arrangement.

9. The method as claimed in claim 2, characterized in that the multiplicity of signals or items of information is determined with a biochip as claimed in claim 8.

10. A nucleotide sequence characterized in that it is chosen from the group consisting of:

a) the reference sequences SEQ ID Nos 235 to 239, and 262 to 271,

b) the sequences complementary to each of the sequences SEQ ID Nos 235 to 239, and 262 to 271, respectively, the complementarity meaning any sequence capable of hybridizing, at a temperature of between 20 and 70°C, in saline solution at a concentration of approximately 0.5 to 1M, with any one of the sequences SEQ ID Nos 235 to 239, and 262 to 271,

c) the sequences homologous to each of the sequences SEQ ID Nos 235 to 239, and 262 to 271, and of the sequences according to b), respectively, the homology meaning any sequence, for example fragment, comprising a series of at least 5 contiguous nucleotides included in any one of said sequences and also a group of two or three nucleotides belonging to a region which has been conserved for all the species of

a group under consideration, and said sequence exhibiting at least 70% identity with said any sequence.

11. A nucleotide sequence characterized in that it consists of a group of 1 to 3 nucleotides included in one of the sequences as claimed in claim 10 and corresponding to a region which has been conserved for all the species of a group under consideration.

12. The nucleotide sequence as claimed in claim 11, characterized in that it consists of the CAA bases at positions 14689-14690-14691 of SEQ ID No. 235 or the CT bases at positions 15076-15077 of SEQ ID No. 236 or the CT bases at positions 15101-15102 of SEQ ID No. 237 or the GC bases at positions 14886-14887 of SEQ ID No. 238 or the ATA bases at positions 14713-14726 of SEQ ID No. 239.

13. The nucleotide sequence as claimed in claim 11, characterized in that it consists of the T base at position 14641 of SEQ ID No. 262 or the A base at position 14778 of SEQ ID No. 263 or the C base at position 15043 of SEQ ID No. 264, or the C base at position 15076 of SEQ ID No. 265, or the C base at position 15101 of SEQ ID No. 266, or the A base at position 15109 of SEQ ID No. 267, or the C base at position 15115 of SEQ ID No. 268, or the C base at position 15239 of SEQ ID No. 269, or of the nucleotide sequence consisting of the T base at position 14519 of SEQ ID No. 270 or the T base at position 14717 of SEQ ID No. 271.

14. A reagent for determining at least one original animal species, comprising a solid support, which may or may not be divided up, to which a nucleotide sequence as claimed in claim 10 is attached.

15. A method for determining a group of original

animal species in a sample liable to contain an ingredient obtained from at least one species belonging to said group of animal species under consideration, characterized in that:

a) a nucleic acid fraction obtained from said sample is provided,

b) at least one reagent comprising a sequence as claimed in claim 10 is provided,

c) the nucleic acid fraction and said reagent are brought into contact, and

d) any signal or item of information resulting from the presence of one of the sequences as claimed in any one of claims 11 to 13, characterizing the presence in said sample of a group of original animal species, is determined by means of detection.

16. The use of the sequences defined in any one of claims 11 to 13, for determining a group of original animal species in a sample liable to contain an ingredient obtained from at least one animal species belonging to said group of animal species under consideration.

17. A method for determining a group of original animal species in a sample liable to contain an ingredient obtained from at least one species belonging to said group of animal species under consideration, characterized in that:

a) a nucleic acid fraction obtained from said sample is provided,

b) the nucleotide sequence(s) characteristic of the group of animal species to be determined is (are) identified,

c) at least one reagent comprising a sequence identified in step b) is provided,

c) the nucleic acid fraction and said reagent are brought into contact, and

d) any signal or item of information resulting from the presence of one of the sequences as claimed in

any one of claims 11 to 13, characterizing the presence in said sample of a group of original animal species, is determined by means of detection.